

SCORE Search Results Details for Application 09391861 and Search Result 20070925_081037_us-09-391-861-5.rag.

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This page gives you Search Results detail for the Application 09391861 and Search Result 20070925_081037_us-09-391-861-5.rag.

[Go Back to previous page](#)

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: September 25, 2007, 08:11:41 ; Search time 62 Seconds
(without alignments)
1440.152 Million cell updates/sec

Title: US-09-391-861-5
Perfect score: 969
Sequence: 1 HPIPDSPLLQFGQQVRQRY.....SSDPLSMVGPSQGRSPSYAS 181

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	969	100.0	181	4	AAU00965	Aau00965 Human Fib
2	969	100.0	209	4	AAB82351	Aab82351 Human JAF
3	969	100.0	209	4	AAU00957	Aau00957 Human Fib
4	969	100.0	209	4	AAB83951	Aab83951 Amino aci.
5	961	99.2	181	9	AEB19074	Aeb19074 Human fib
6	959	99.0	181	9	AEB19069	Aeb19069 Human fib
7	959	99.0	181	9	AEB55174	Aeb55174 Human fib
8	959	99.0	181	9	AED28265	Aed28265 Mature hu
9	959	99.0	181	9	AEE39711	Aee39711 Human fib
10	959	99.0	181	10	AEG40944	Aeg40944 Mature hu
11	959	99.0	181	10	AEG36157	Aeg36157 Human fib
12	959	99.0	181	10	AEI54357	Aei54357 Wild-type
13	959	99.0	181	10	AEJ43843	Aej43843 Human mat
14	959	99.0	182	10	AEH50993	Aeh50993 Human fib
15	959	99.0	208	4	AAE05078	Aae05078 Human fib
16	959	99.0	208	5	AAU83630	Aau83630 Human PRO
17	959	99.0	208	5	ABG32358	Abg32358 Human fib
18	959	99.0	208	5	AAE17601	Aae17601 Human ext
19	959	99.0	208	5	ADY31818	Ady31818 Novel hum
20	959	99.0	208	6	ABU80777	Abu80777 Human PRO
21	959	99.0	208	6	ABO33743	Abo33743 Novel hum
22	959	99.0	208	6	ABU82086	Abu82086 Novel hum
23	959	99.0	208	6	ABP96156	Abp96156 Human fib
24	959	99.0	208	6	ABJ72266	Abj72266 Human PRO
25	959	99.0	208	6	ABJ72394	Abj72394 Human PRO
26	959	99.0	208	6	ABO34289	Abo34289 Human sec
27	959	99.0	208	7	ADA37038	Ada37038 Human fib
28	959	99.0	208	7	ABJ72096	Abj72096 Human mem
29	959	99.0	208	7	ADB83568	Adb83568 Novel hum
30	959	99.0	208	7	ADB80674	Adb80674 Novel hum
31	959	99.0	208	7	ADB73215	Adb73215 Novel hum
32	959	99.0	208	7	ADB78297	Adb78297 Novel hum
33	959	99.0	208	7	ADB84945	Adb84945 Human PRO
34	959	99.0	208	7	ADB78051	Adb78051 Novel hum
35	959	99.0	208	7	ADB87117	Adb87117 Human PRO
36	959	99.0	208	7	ADB84699	Adb84699 Human PRO
37	959	99.0	208	7	ADB83814	Adb83814 Novel hum
38	959	99.0	208	7	ADB72969	Adb72969 Novel hum
39	959	99.0	208	7	ADC36807	Adc36807 Human PRO
40	959	99.0	208	7	ADC21797	Adc21797 Human PRO
41	959	99.0	208	7	ADC49828	Adc49828 Novel hum
42	959	99.0	208	7	ADC49027	Adc49027 Novel hum
43	959	99.0	208	7	ADC49544	Adc49544 Novel hum
44	959	99.0	208	7	ADC47405	Adc47405 Novel hum
45	959	99.0	208	7	ADC47150	Adc47150 Novel hum

ALIGNMENTS

RESULT 1

AAU00965

ID AAU00965 standard; protein; 181 AA.

XX

AC AAU00965;

XX
DT 24-MAY-2001 (first entry)
XX
DE Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.
XX
KW Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
KW neurodegenerative disease; haematopoietic cell reconstitution; cachexia;
KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
KW multiple sclerosis; short stature; delayed maturation; excessive growth;
KW acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
KW androgen target organ abnormality; respiratory distress syndrome; stroke;
KW cancer; atherosclerosis; hypercholesterolemia; osteoporosis; baldness;
KW osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
KW decreased stamina; decreased cardiac function; immune system dysfunction;
KW Parkinson's disease; Alzheimer's disease; decreased cognitive function;
KW senile dementia; human.
XX
OS Homo sapiens.
XX
PN WO200118172-A2.
XX
PD 15-MAR-2001.
XX
PF 05-SEP-2000; 2000WO-US024373.
XX
PR 07-SEP-1999; 99US-00391861.
PR 23-AUG-2000; 2000US-00644052.
XX
PA (AMGE-) AMGEN INC.
XX
PI Thomason AR, Liu B;
XX
DR WPI; 2001-226743/23.
XX
PT Novel isolated fibroblast growth factor-like polypeptide useful for
PT treating, preventing or ameliorating cirrhosis, inflammatory bowel
PT disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
PT osteoporosis.
XX
PS Claim 14; Page 116-117; 138pp; English.
XX
CC The sequence represents a fragment of a fibroblast growth factor-like
CC (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid
CC play a role in modulating body growth, maturation or life-span. They are
CC also useful for treating, preventing or ameliorating disorders such as
CC cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease,
CC diabetes, obesity, gastrointestinal abnormalities, neurodegenerative
CC diseases, damage to renal tubules as a result of acute tubular necrosis,
CC haematopoietic cell reconstitution following chemotherapy, wasting
CC syndromes (e.g., cancer associated cachexia), damage to the corneal
CC epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
CC stature, delayed maturation, excessive growth (e.g. acromegaly),
CC premature maturation, alopecia, abnormalities of androgen target organs,
CC bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
CC of the eye or other tissues, atherosclerosis, hypercholesterolemia,
CC stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
CC baldness, wrinkles, increased fatigue, decreased stamina, decreased
CC cardiac function, immune system dysfunction, cancer, Parkinson's disease,
CC senile dementia, Alzheimer's disease, and decreased cognitive function

XX

SQ Sequence 181 AA;

Query Match 100.0%; Score 969; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 3.7e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTTEAHLEIREDTGTVGGAADQSPESLLQLKALKP 60
 |||||||
 Db 1 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTTEAHLEIREDTGTVGGAADQSPESLLQLKALKP 60

Qy 61 GVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 120
 |||||||
 Db 61 GVIQILGVKTSRFLCQRPDGALY GSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 120

Qy 121 NKSPHRDPAPRGPARFLPLPGLPPAPPEPPGILAPQPPDVGS SDPLSMVGPSQGRSPSYA 180
 |||||||
 Db 121 NKSPHRDPAPRGPARFLPLPGLPPAPPEPPGILAPQPPDVGS SDPLSMVGPSQGRSPSYA 180

Qy 181 S 181
 |
 Db 181 S 181

RESULT 2

AAB82351

ID AAB82351 standard; protein; 209 AA.

XX

AC AAB82351;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human JAFFA protein.

XX

KW JAFFA; human; fibroblast growth factor; diagnosis; therapy; cancer;
 KW autoimmune disease; cytostatic; immunosuppressive; neuroprotective.

XX

OS Homo sapiens.

XX

FT	Key	Location/Qualifiers
FT	Peptide	1. .28
FT		/label= Signal_peptide
FT	Modified-site	6. .9
FT		/note= "predicted casein kinase II phosphorylation site"
FT	Modified-site	12. .17
FT		/note= "N-myristoylation"
FT	Modified-site	20. .25
FT		/note= "N-myristoylation"
FT	Protein	29. .209
FT		/label= Mature_protein
FT	Domain	60. .140
FT		/note= "fibroblast growth factor domain"
FT	Modified-site	67. .72
FT		/note= "N-myristoylation"
FT	Modified-site	95. .100
FT		/note= "N-myristoylation"
FT	Modified-site	98. .100
FT		/note= "protein kinase C predicted phosphorylation site"
FT	Modified-site	108. .113
FT		/note= "N-myristoylation"
FT	Modified-site	122. .125

FT /note= "predicted casein kinase II phosphorylation site"
 FT Modified-site 122..124
 FT /note= "protein kinase C predicted phosphorylation site"
 XX
 PN WO200138357-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032181.
 XX
 PR 22-NOV-1999; 99US-00444165.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Khodadoust MM;
 XX
 DR WPI; 2001-355881/37.
 DR N-PSDB; AAF90326, AAF90327.
 XX
 PT Isolated JAFFA nucleic acid molecules which encode novel fibroblast
 PT growth factor family members (JAFFA) are useful for developing novel
 PT diagnostic and therapeutic agents for JAFFA-associated disorders such as
 PT cancers.
 XX
 PS Claim 2; Fig 1; 137pp; English.
 XX
 CC The present sequence is that of human JAFFA, a novel member of the
 CC fibroblast growth factor family. Analysis of rare sequences in the
 CC Millennium database led to the identification of an expressed sequence
 CC tag from a human prostate tumour library which coded for a novel
 CC hypothetical signal peptide. Further analysis led to the identification
 CC of JAFFA. The invention provides JAFFA polypeptides, polynucleotides and
 CC anti-JAFFA antibodies. It also provides antisense nucleic acid molecules,
 CC recombinant expression vectors, host cells and transgenic animals. JAFFA
 CC proteins may be useful for developing novel diagnostic and therapeutic
 CC agents for JAFFA-associated disorders such as cancers and other disorders
 CC which demonstrate ABO(H) blood group disorders and for controlling
 CC cellular proliferative and/or differentiative disorders. The JAFFA
 CC nucleic acid and protein may be used to treat and/or diagnose a variety
 CC of immune disorders such as autoimmune disease and multiple sclerosis.
 CC The proteins may also be used to screen for naturally occurring JAFFA
 CC substrates, to screen for drugs or compounds which modulate JAFFA
 CC activity, and to raise anti-JAFFA antibodies, which can be used to detect
 CC and isolate JAFFA proteins, regulate the bioavailability of JAFFA
 CC proteins and modulate JAFFA activity
 XX
 SQ Sequence 209 AA;

Query Match 100.0%; Score 969; DB 4; Length 209;
 Best Local Similarity 100.0%; Pred. No. 4.4e-76;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTTEAHLEIREDGTVGGAADQSPESLLQLKALKP 60
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 29 HPIPDSSPLLQFGGQVRQRYLYTDDAQQTTEAHLEIREDGTVGGAADQSPESLLQLKALKP 88
 Qy 61 GVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 89 GVIQILGVKTSRFLCQRPDGALYGSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPG 148
 Qy 121 NKSPHRDPAPRGPAPFLPLPGLPPAPPEPPGILAPQPPDVGSSDPLSMVGPSQGRSPSYA 180